

Snedden

re-run

# 1600
16

RAW SEQUENCE LISTING

DATE: 07/14/2003

PATENT APPLICATION: US/09/997,610

TIME: 11:46:52

Input Set : A:\US09997610.raw

Output Set: N:\CRF4\07142003\I997610.raw

1 <110> APPLICANT: Fox, Brian
 2 Holloway, James L.
 3 <120> TITLE OF INVENTION: ADIPOCYTE COMPLIMENT RELATED PROTEIN
 4 ZACRP13
 5 <130> FILE REFERENCE: 00-96
 6 <140> CURRENT APPLICATION NUMBER: US/09/997,610
 7 <141> CURRENT FILING DATE: 2001-11-29
 8 <150> PRIOR APPLICATION NUMBER: US 60/253,924
 9 <151> PRIOR FILING DATE: 2000-11-29
 10 <160> NUMBER OF SEQ ID NOS: 7
 11 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1381
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Homo sapiens
 17 <220> FEATURE:
 18 <221> NAME/KEY: CDS
 19 <222> LOCATION: (2)...(1381)
 20 <400> SEQUENCE: 1

21 g ata gtg gtc ata cct gtc tta ata acg gca gtc att gag cat gta gaa 49
 22 Ile Val Val Ile Pro Val Leu Ile Thr Ala Val Ile Glu His Val Glu
 23 1 5 10 15
 24 gtt gct gga cct cca gca cac ccc agg ccc cca gaa gaa gtg ggg cct 97
 25 Val Ala Gly Pro Pro Ala His Pro Arg Pro Pro Glu Glu Val Gly Pro
 26 20 25 30
 27 cct ggt gca cca ggt tta cca caa tat aca gga gaa ata agt gaa atg 145
 28 Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr Gly Glu Ile Ser Glu Met
 29 35 40 45
 30 aca aaa tgc ccc tgt cct gat ata gaa agg tca gcc ttt act gtg aag 193
 31 Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys
 32 50 55 60
 33 ctc agt gga aaa ctt cct ctt cct ttc aag ccc atc atc ttc aca ggg 241
 34 Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys Pro Ile Ile Phe Thr Gly
 35 65 70 75 80
 36 gtc ctg tac aat gcc cag agg gat tta aag gag gcc atg gga gtc ttt 289
 37 Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys Glu Ala Met Gly Val Phe
 38 85 90 95
 39 gct tgc agg gtg cct ggg aat tac tac tcc agc ttt gat gtt gag ctg 337
 40 Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser Ser Phe Asp Val Glu Leu
 41 100 105 110
 42 cat cat tgc aag gtg aat att tgg cta atg agg aag caa att ttg gct 385
 43 His His Cys Lys Val Asn Ile Trp Leu Met Arg Lys Gln Ile Leu Ala
 44 115 120 125

ENTERED

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45	aat aag gaa gaa att tct aag cag caa agc att caa gag gtg act tgg	433
46	Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser Ile Gln Glu Val Thr Trp	
47	130 135 140	
48	gtg ctg tta aag gca ttc agt ttc ata agg gag gca gag cat aag agt	481
49	Val Leu Leu Lys Ala Phe Ser Phe Ile Arg Glu Ala Glu His Lys Ser	
50	145 150 155 160	
51	tca gaa aat ttg cac cct gac aat gtg ata aaa aag aaa aac cca ttt	529
52	Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe	
53	165 170 175	
54	tct gag ggg aaa ttc aag ctg gct gca gaa att tgc ata tgt aat gag	577
55	Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu	
56	180 185 190	
57	gag ctg aat gtt aat cct caa gac aat ggg gaa aat atc tcc tgg aca	625
58	Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr	
59	195 200 205	
60	tgt cag agg tct tca cag cag tcc atc aaa tca ctg gcc tgg agg cct	673
61	Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro	
62	210 215 220	
63	agg aga aaa tgg ttt tgt ggg aca ggc cca ggg tcc ctg tgc tgt gtg	721
64	Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val	
65	225 230 235 240	
66	cag cct aga gac ttg gtg ccc tgt gtc cca gtt aat tca gct gtg gct	769
67	Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala	
68	245 250 255	
69	tca gag ggt gca agc ccc aag cct tgg cag ctt cca agt ggt gtt gag	817
70	Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu	
71	260 265 270	
72	cct gtg ggt gca aag aag tca aga att gag gtt tgg gaa cct cca atc	865
73	Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile	
74	275 280 285	
75	aga ttt cag aag ata tat gga aac ccc tgg atg ccc agg cag aag ttt	913
76	Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe	
77	290 295 300	
78	gct gta ggg gtg ggg tcc tca tgg aga acc tct gca agg gta gta caa	961
79	Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln	
80	305 310 315 320	
81	aag gga aat gtt ggg tgg gag ccc cca cac aga gtc ccc agt ggg gct	1009
82	Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala	
83	325 330 335	
84	cca tct agt aga gct gtg aga aga agt cca cca tcc tcc aga ctc cag	1057
85	Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln	
86	340 345 350	
87	aag ggt aga tcc act gac agc ttg cag cat gtg cct gaa aaa tcc aca	1105
88	Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr	
89	355 360 365	
90	gac act cag tgc cag cct gtg aaa gca gca ggg atg gag tct gta ccc	1153
91	Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro	
92	370 375 380	
93	tac aaa acc gta gtg gca gag ctg acc aag acc gtg gga atc tac ctc	1201

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94   Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu
95   385                               390                               395                               400
96   ttg cat tgt cat gac ctg gac gtg aga cat gga gtc aaa aga gat cat      1249
97   Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His
98                               405                               410                               415
99   ttt gga gct tta aga ttt gac tgc ccc act gga ttt cgg act tat atg      1297
100   Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met
101                               420                               425                               430
102   ggg ccc gta ccc ctt tgt ttt ggc caa ttt ttt cca ttt gga act gcc      1345
103   Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala
104                               435                               440                               445
105   gta ttt acc caa tgc ctg tac ctc cat tgt atg tag      1381
106   Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met *
107   450                               455

109 <210> SEQ ID NO: 2
110 <211> LENGTH: 459
111 <212> TYPE: PRT
112 <213> ORGANISM: Homo sapiens
113 <400> SEQUENCE: 2
114   Ile Val Val Ile Pro Val Leu Ile Thr Ala Val Ile Glu His Val Glu
115   1                               5                               10                               15
116   Val Ala Gly Pro Pro Ala His Pro Arg Pro Pro Glu Glu Val Gly Pro
117                               20                               25                               30
118   Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr Gly Glu Ile Ser Glu Met
119   35                               40                               45
120   Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys
121   50                               55                               60
122   Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys Pro Ile Ile Phe Thr Gly
123   65                               70                               75                               80
124   Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys Glu Ala Met Gly Val Phe
125   85                               90                               95
126   Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser Ser Phe Asp Val Glu Leu
127   100                              105                              110
128   His His Cys Lys Val Asn Ile Trp Leu Met Arg Lys Gln Ile Leu Ala
129   115                              120                              125
130   Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser Ile Gln Glu Val Thr Trp
131   130                              135                              140
132   Val Leu Leu Lys Ala Phe Ser Phe Ile Arg Glu Ala Glu His Lys Ser
133   145                              150                              155                              160
134   Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe
135   165                              170                              175
136   Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu
137   180                              185                              190
138   Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr
139   195                              200                              205
140   Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro
141   210                              215                              220
142   Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val
143   225                              230                              235                              240

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```

144      Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala
145                      245                      250                      255
146      Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu
147                      260                      265                      270
148      Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile
149                      275                      280                      285
150      Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe
151                      290                      295                      300
152      Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln
153      305                      310                      315                      320
154      Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala
155                      325                      330                      335
156      Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln
157                      340                      345                      350
158      Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr
159                      355                      360                      365
160      Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro
161      370                      375                      380
162      Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu
163      385                      390                      395                      400
164      Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His
165                      405                      410                      415
166      Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met
167                      420                      425                      430
168      Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala
169                      435                      440                      445
170      Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met
171                      450                      455

173 <210> SEQ ID NO: 3
174 <211> LENGTH: 1377
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Degenerate polynucleotide encoding a polypeptide
179      of SEQ ID NO:2
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181 <222> LOCATION: (1)...(1377)
182 <223> OTHER INFORMATION: Each n is independently A, T, G, or C.
W--> 183 <221> misc_feature
184 <222> LOCATION: (1)...(1377)
185 <223> OTHER INFORMATION: n = A,T,C or G
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W--> 187      athgtngtna thcngtnyt nathacngcn gtnathgarc aygtngargt ngcnggncn      60
188      ccngcncayc cmngnccncc ngargargtn ggncncncng gngcncncng nytnccncar      120
189      tayacngng arathwsnga ratgacnaar tgyccntgyc cngayathga rmgnwsngcn      180
190      ttyacngtna arytnwsngg naarytnccn ytnccnttya arccnathat httyacnggn      240
191      gtnyntaya aygcncarmg ngayytnaar gargcnatgg gngtnttygc ntgymngn      300
192      ccnggnaayt aytaywsnws nttygaygtg garytncayc aytgyaargt naayathtgg      360
193      ytnatgmnga arcarathyt ngcnaayaar gargarathw snaarcarca rwsnathcar      420

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```

194      gargtnacnt gggtnytnyt naargcntty wsnttyathm gngargcnga rcayaarwsn      480
195      wsngaraaay tncayccnga yaaygtnath aaraaraara ayccnttyws ngarggnaar      540
196      ttyaarytng cngcngarat htgyathtgy aaygargary tnaaygtnaa yccncargay      600
197      aayggngara ayathwsntg gacntgycar mgnwsnwsnc arcarwsnat haarwsnytn      660
198      gcntggmgnc cnmgnmgnaa rtggttytgy ggnacnggnc cnggnwsnyt ntgytgygtn      720
199      carccnmngn ayytngtncc ntgygtncn gtnaaywsng cngtngcnws ngarggngcn      780
200      wsncnaarc cntggcaryt nccnwsnggn gtngarccng tnggngcnaa raarwsnmgn      840
201      athgargtnt gggarccncc nathmgntty caraaratht ayggnaaycc ntggatgccn      900
202      mgncaraart tygcngtngg ngtnngnwsn wsntggmgna cnwsngcnmg ngtngtncar      960
203      aarggnaayg tnggntggga rccncncay mgngtnccnw snggngcncc nwsnwsnmgn      1020
204      gcngtnmgm gnwsnccncc nwsnwsnmgn ytncaraarg gnmgnwsnac ngaywsnytn      1080
205      carcaygtnc cngaraarws nacngayaen cartgyarc cngtnaargc ngcnggnatg      1140
206      garwsngtnc cntayaarac ngtngtngcn garytnacna aracngtngg nathtayytn      1200
207      ytncaytgyc aygayytnga ygtnmgnay gngtngaarm gngaycaytt yggngcnyn      1260
208      mgnttygayt gyccnacngg nttymgnacn tayatgggnc cngtnccnyt ntgyttygg      1320
209      carttytgc cnttyggnac ngcngtntty acncartggy tntayytnca ytgyatg      1377
211 <210> SEQ ID NO: 4
212 <211> LENGTH: 31
213 <212> TYPE: PRT
214 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Aromatic motif
W--> 217 <221> NAME/KEY: VARIANT
218 <222> LOCATION: (2)...(6)
219 <223> OTHER INFORMATION: Each Xaa is any amino acid residue
W--> 220 <221> VARIANT
221 <222> LOCATION: (7)...(7)
222 <223> OTHER INFORMATION: Xaa is asparagine or aspartic acid
W--> 223 <221> VARIANT
224 <222> LOCATION: (8)...(11)
225 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
W--> 226 <221> VARIANT
227 <222> LOCATION: (12)...(12)
228 <223> OTHER INFORMATION: Xaa is phenylalanine, tyrosine, tryptophan, or
229      leucine
W--> 230 <221> VARIANT
231 <222> LOCATION: (13)...(18)
232 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
W--> 233 <221> VARIANT
234 <222> LOCATION: (20)...(24)
235 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
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237 <222> LOCATION: (26)...(26)
238 <223> OTHER INFORMATION: Xaa is any amino acid residue
W--> 239 <221> VARIANT
240 <222> LOCATION: (28)...(31)
241 <223> OTHER INFORMATION: Each Xaa is independently any amino acid residue
W--> 242 <400> 4
W--> 243      Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 6,9,15,18,21,27,30,33,45,51,54,57,60,63,66,72,75,78,81,90,93
Seq#:3; N Pos. 96,99,102,105,108,111,114,117,126,129,138,147,156,162,174
Seq#:3; N Pos. 177,180,186,189,195,198,201,207,210,213,216,225,237,240,243
Seq#:3; N Pos. 246,255,261,267,276,282,285,291,297,300,303,306,318,321,330
Seq#:3; N Pos. 336,351,363,369,381,384,402,414,426,429,435,438,441,447,453
Seq#:3; N Pos. 462,468,480,483,492,498,507,525,531,537,549,552,555,582,588
Seq#:3; N Pos. 594,606,618,624,633,636,639,648,657,660,663,669,672,675,678
Seq#:3; N Pos. 693,696,699,702,705,708,711,720,726,729,735,738,741,747,750
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Seq#:3; N Pos. 813,819,822,825,828,837,840,849,858,861,867,885,891,900,903
Seq#:3; N Pos. 915,918,921,924,927,930,933,939,942,945,948,951,954,957,966
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Seq#:3; N Pos. 1020,1023,1026,1029,1032,1035,1038,1041,1044,1047,1050,1053
Seq#:3; N Pos. 1062,1065,1068,1071,1077,1080,1089,1092,1101,1104,1110,1122
Seq#:3; N Pos. 1125,1131,1134,1137,1146,1149,1152,1161,1164,1167,1170,1176
Seq#:3; N Pos. 1179,1185,1188,1191,1200,1203,1218,1224,1227,1233,1236,1242
Seq#:3; N Pos. 1254,1257,1260,1263,1275,1278,1281,1287,1290,1299,1302,1305
Seq#:3; N Pos. 1308,1311,1320,1332,1338,1341,1344,1347,1353,1362,1368
Seq#:4; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,20,21,22,23,24
Seq#:4; Xaa Pos. 26,28,29,30,31
Seq#:7; N Pos. 6,15,21,24,30,33,36,42,45,63,72,81,84,87,93,96,99,102,105
Seq#:7; N Pos. 111,117,120,126,129,132,147,150,156,162,171,174,180,189,192
Seq#:7; N Pos. 207,210,216,219,222,225,228,234,237,240,249,252,255,258,261
Seq#:7; N Pos. 264,267,270,273,276,279,288,291,297,300,303,306,309,315,321
Seq#:7; N Pos. 324,327,333,339,345,348,354,360,363,369,372,375,381,384,387
Seq#:7; N Pos. 399,405,408,411,414,417,420,426,429,432,435,444,447,450,453
Seq#:7; N Pos. 456,459,462,465,468,471,480,483,492,501,510,516,528,531,534
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Seq#:7; N Pos. 1194,1203,1212,1215,1221,1239,1245,1254,1257,1269,1272,1275
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Seq#:7; N Pos. 1407,1416,1419,1422,1425,1431,1434,1443,1446,1455,1458,1464
Seq#:7; N Pos. 1476,1479,1485,1488,1491,1500,1503,1506,1515,1518,1521,1524
Seq#:7; N Pos. 1530,1533,1539,1542,1545,1554,1557,1572,1578,1581,1587,1590
Seq#:7; N Pos. 1596,1608,1611,1614,1617,1629,1632,1635,1641,1644,1653,1656
Seq#:7; N Pos. 1659,1662,1665,1674,1686,1692,1695,1698,1701,1707,1716,1722

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\US09997610.raw
Output Set: N:\CRF4\07142003\I997610.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:3; Line(s) 187,188,189,190,191,192,193,194,195,196,197,198,199,200,201

Seq#:3; Line(s) 202,203,204,205,206,207,208,209

Seq#:7; Line(s) 457,458,459,460,461,462,463,464,465,466,467,468,469,470,471

Seq#:7; Line(s) 472,473,474,475,476,477,478,479,480,481,482,483,484,485

VERIFICATION SUMMARY

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Input Set : A:\US09997610.raw

Output Set: N:\CRF4\07142003\I997610.raw

L:180 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:183 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:186 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:341 Repeated in SeqNo=3
L:217 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:220 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:223 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:226 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:230 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:233 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:236 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:239 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:242 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
M:341 Repeated in SeqNo=4
L:453 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:456 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
M:341 Repeated in SeqNo=7

gcttgtgac cgcccgccctc ggccctcccaa agtgctggga ttacaggcgt gagccacagc
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